

FIGURE 1

Anti-OX40 phage SC02009

Anti-OX40 phage SC02008

Ctrl phage

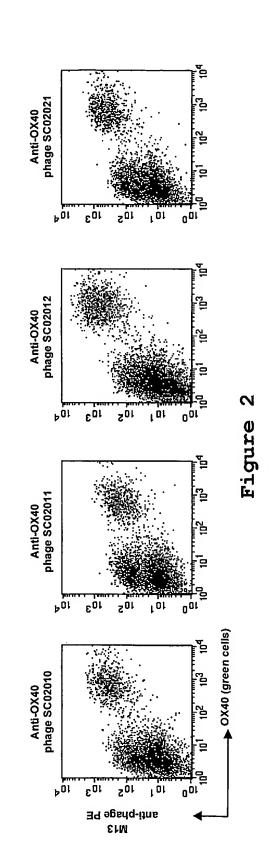
E₀₁

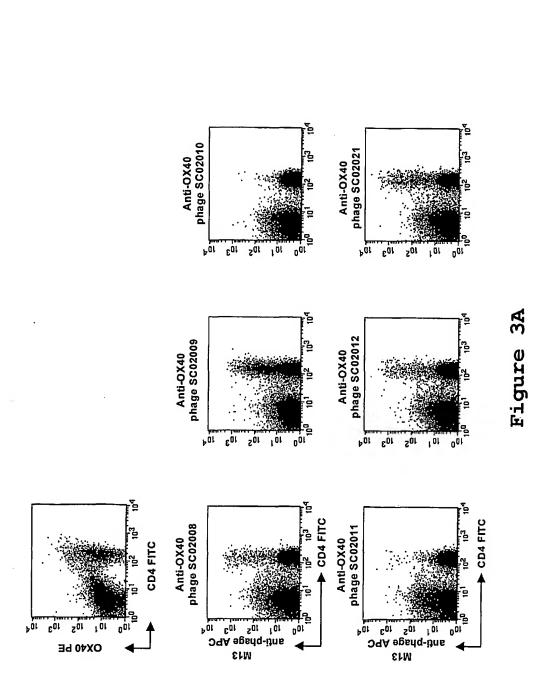
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E₀₁

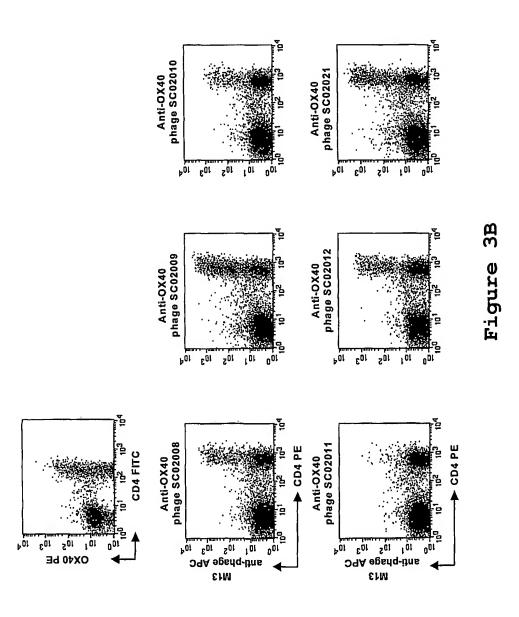
M13 anti-phage PE 5

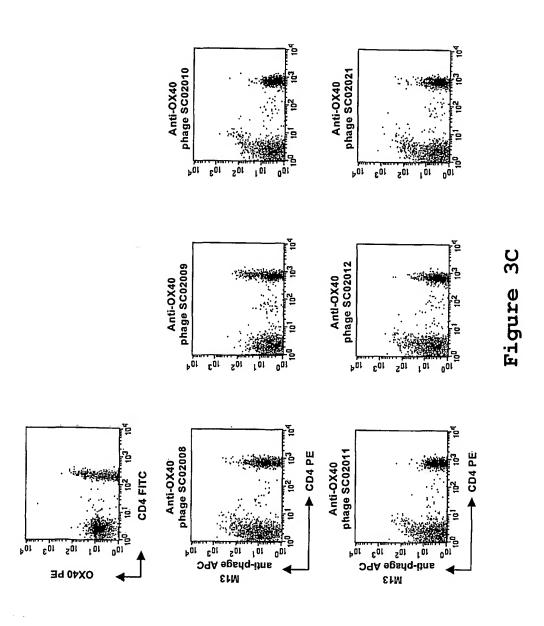
OX40 (green cells)

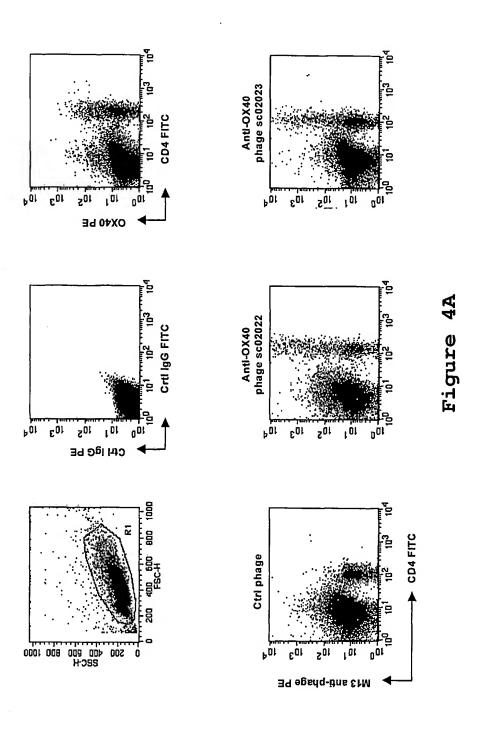




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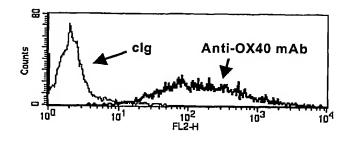


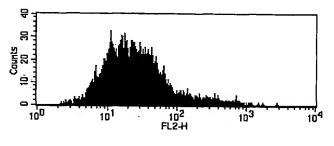




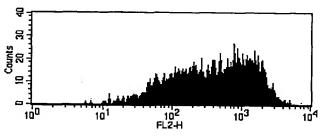


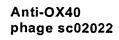
Perc6 OX40 transfectant

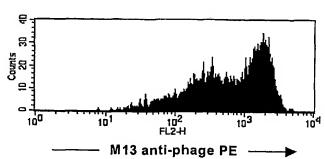




Ctrl phage







Anti-OX40 phage sc02023

Figure 4B

853

Anti-human OX40R scFv SC02008

	NCOI
143	M A E V Q L V E S G G G L V Q P G G S L R CCATGGCTGAGGTGCAGCTGGAGGTCCCTGAG
214	L S C A A S G F T F S N Y T M N W V R Q A P G ACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAACTACACGATGAACTGGGTCCGCCAGGCGCCCGGGA
285	K G L E W V S A I S G S G G S T Y Y A D S V K G AGGGGCTGGAGTGGTCTCAGCTATTAGTGGTAGTGGTAGCACATACTACGCAGACTCCGTGAAGGGC
356	R F T I S R D N S K N T L Y L Q M N S L R A E D CGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGA
427	T A V Y Y C A K D R Y S Q V H Y A L D Y W G Q CACGGCCGTGTATTACTGTGCCAAAGACCGCTACTCCCAGGTGCACTACGCGTTGGATTACTGGGGCCAGG
498	G T L V T V L E G T G G S G T G S G T G T S E GCACCCTGGTGACCGTGCTCGGGGTACCGGAGGTTCCGGCGGAACCGGGTCTGGGACTGGTACGAGCGAG
569	L D I Q M T Q S P D S L P V T P G E P A S I S C CTCGACATCCAGATGACGCAGTCTCCAGACTCACTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTG
640	R S S Q S L L H S N G Y N Y L D W Y L Q K A G CAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGGCAGGGC
711	Q S P Q L L I Y L G S N R A S G V P D R F S G S AGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGT
782	G S G T D F T L K I S R V E A E D V G V Y Y C C GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGGGGGGGG
	NotI
853	Q Y Y N H P T T F G Q G T K L E I K R A A GCAGTACTACAACCACCCGACGACCTTCGGCCAGGGCACCAAACTGGAAATCAAACGCGCGGCCGC

	NcoI
143	M A E V Q L V E S G G L CCATGGCTGAGGTGCAGCTGGGGGAGGCTTG
214	V Q P G G S L R L S C A A S G F T F S G Y S M N GTCCAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACCTTCAGCGGCTACTCTATGAA
285	W V R Q A P G K G L E W V G R T R N K A N S Y CTGGGTCCGCCAGGCGCCGGGAAGGGGCTGGAGTGGCTGGC
356	T T E Y A A S V K G R F T I S R D D S K N S L Y CCACAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATTCAAAGAACTCACTGTAT
427	L Q M N S L R A E D T A V Y Y C A K <u>D R Y V N T</u> CTGCAAATGAACAGTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCCAAAGACCGCTACGTCAACAC
498	S N A F D Y W G Q G T L V T V L E G T G G S G GTCGAACGCGTTCGATTACTGGGGCCAGGGCACCCTGGTGACCGTGCTCGAGGGTACCGGAGGTTCCGGCG
569	G T G S G T G T S E L D I Q M T Q S P D S L P V GAACCGGGTCTGGGACTGGTACGAGGTGGGGGGGGTCCAGACTCACTGCCCGTC
640	T P G E P A S I S C R S S Q S L L H S N G Y N Y ACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGATCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTA
711	L D W Y L Q K P G Q S P Q L L I Y L G S N R A TTTGGATTGGTACCTGCAGAGCCAGGCCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCT
782	S G V P D R F S G S G S G T D F T L K I S R V E CCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAG
853	A H H V G V Y Y C Q Q Y P L G P P T F G Q G T K GCTCACCATGTTGGGGTTTATTACTGCCAGCAGTACCCGCTGGGCCCGCCC
	Noti
	L E I K R A A
924	ACTGGAAATCAAACGCGCGCCGC

	NcoI
	~~~~
72	M A E V Q L V CCATGGCTGAGGTGCAGCTGGTGG
143	E S G G G L I Q P G G S L R L S C A A S G F T F AGTCTGGGGGGGGCTTGATCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTC
214	S G Y P M N W V R Q A P G K G L E W V A V I S Y AGCGGCTACCCTATGAACTGGGTCCGCCAGGCGCCCGGGAAGGGGCTGGAGTGGGTGG
285	D G S N K Y Y A D S V K G R F T I S R D N S K TGATGGAAGTAATAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGA
356	N T L Y L Q M N S L R A E D T A V Y Y C A R $\underline{D}$ M ACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACAGCCGTGTATTACTGTGCAAGAGACATG
427	$\frac{\texttt{S} \ \ \texttt{G} \ \ \texttt{F} \ \ \texttt{H} \ \ \texttt{E} \ \ \texttt{F} \ \ \texttt{D} \ \ \texttt{Y} \ \ \texttt{W} \ \ \texttt{G} \ \ \texttt{Q} \ \ \texttt{G} \ \ \texttt{T} \ \ \texttt{L} \ \ \texttt{V} \ \ \texttt{T} \ \ \texttt{V} \ \ \texttt{L} \ \ \texttt{E} \ \ \texttt{G} \ \ \texttt{T} \ \ \texttt{G} \ \ \ \texttt{G} \ \ \ \texttt{G} \ \ \ \texttt{G} \ \ \texttt{G} \ \ \ \ \texttt{G} \ \ \ \ \texttt{G} \ \ \ \ \texttt{G} \ \ \ \ \ \texttt{G} \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$
498	G G T G S G T G T S E L T Q S P S S L S A S V CGGCGGAACCGGGTCTGGGACTGGTACGAGCGAGCTCACCCAGTCTCCATCCTCCTGTCTGCATCTGTAG
569	G D R V T I T C R A S Q S I S S Y L N W Y Q Q K GAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTACTTAAATTGGTATCAGCAGAAA
640	P G K A P K L L I Y A A S S L Q S G V P S R F S CCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAG
711	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
	NotI
	Y C Q Q S Y S T P P T F G Q G T K V E I K R A A
782	ACTGTCAACAGAGTTACAGTACCCCTCCAACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTGCGGCC

	NcoI
143	M A E V Q L V E S G G V V Q P G R CCATGGCTGAGGTGCAGCTGGTGGAGGTCTGGGAGGGT
214	S L R L S C A A S G F T F S D Y T M N W V R Q A CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGCGATGAACTGGGTCCGCCAGGCG
285	P G K G L E W V S S I S G G S T Y Y A D S R K G CCCGGGAAGGGCTGGAGTGGTCTCATCCATTAGTGGTGGTAGCACATACTACGCAGACTCCAGGAAGGG
356	R F T I S R D N S K N T L Y L Q M N N L R A E CAGATTCACCATCTCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAACCTGAGAGCTGAGG
427	D T A V Y Y C A R D R Y F R Q Q N A F D Y W G Q ACACGGCCGTGTATTACTGTGCAAGAGCCGCTACTTCAGGCAGAACGCGTTCGATTACTGGGGCCAG
498	G T L V T V L E G T G G S G T G S G T G T S E GGCACCCTGGTGACGTGCTCGAGGGTACCGGAGCTTCCGGCGGAACCGGGTCTGGGACTGGTACGAGCGA
569	L D I Q M T Q S P V T L P V T P G E P A S I S GCTCGACATCCAGATGACTCAGTCTCCAGTCACCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCT
640	C R S S Q S L L H S N G Y N Y L D W Y L Q K P G GCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGG
711	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
782	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
853	Noti QQYLTAPPTFGQGTKLEIKRAA AGCAGTACCTCACGGCCCCCCCCCCCCCCCCCCCCCACCTAACTGGAAATCAAACGCGCGCCCCC



	Ncol
	~~~~
72	M A E V Q L V E CCATGGCTGAAGTGCAGCTGGTGGA
	S G G G L V K P G G S L R L S C A A S G F T F S AAGCGGCGGCGGCTGAGCCGGGTGCAGCCTGCGCCTGAGCGCCTGAGCGGCTTCACCTTTA
214	N D S M N W M R Q A P G K G L E W V A N I N Q GCAACGACTCGATGAACTGGATGCGCCAGGCCCCGGGCAAAGGCCTCGAATGGGTGGCCAATATCAATCA
285	D G N E K Y Y A D S V K G R F T I S R D N S K N GATGGCAACGAAAAATATTACGCCGACTCTGTCAAAGGCCGCTTCACCATCAGTCGCGATAACTCCAAAAA
356	S L Y L Q M N S L R D E D T A L Y Y C A R $\frac{A}{A}$ CTCCCTGTACCTGCAGATGAACAGCCTGCGCGACGAAGATACCGCCCTGTACTACTGCGCACGCGCCCGCG
427	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
498	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
569	A S V G D R V T I T C R A S Q N V S N Y L T W CGCCTCCGTGGCCGACCGCGTGACCATCACCTGCCGCGCCAGCCA
640	Y Q Q K P G K A G K L L I Y A A S S L Q S G V P ACCAGCAGAAACCGGGCAAACTGCTGATTTACGCCGCCAGCAGCCTCCAAAGCGGCGTGCCG
711	S R F S G S G S G T D F T L T I S S L Q P E D F TCTAGATTCAGTGGCTCCGGCACCGATTTTACCCTGACCATCAGCAGCCTGCAGCCGGAAGATTT
782	A T Y Y C Q Q S Y F N P A T F G Q G T K L E I CGCTACCTACTATTGTCAGCAGTCCTACTTCAACCCGGCGACCTTCGGCCAGGGCACCAAACTGGAAATCA
	Noti
853	K R A A AACGCGGGCCGC

Figure 9

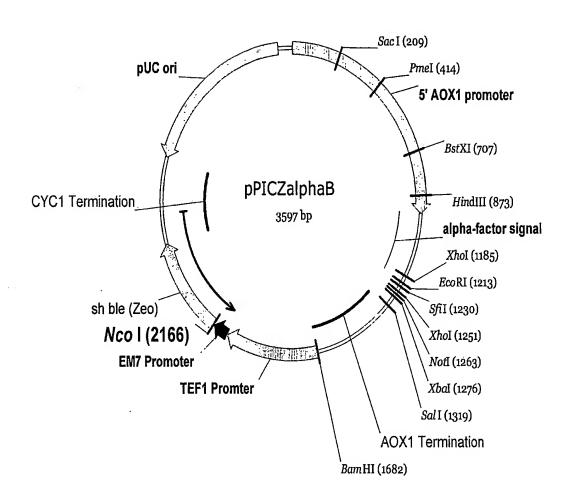
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214	V Q P R G S L R L S C A A S G F T F S S Y A M N GTACAGCCTAGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTACGCGATGAA
285	W V R Q A P G K G L E W V A V I S Y D G S N K CTGGGTCCGCCAGGCCCCGGGAAGGGGCTGGAGTGGCTGTATATCATATGATGAAGCAATAAAT
356	Y Y A D S V K G R F T I S R D N S K N T L Y L Q ACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACACGCTGTATCTGCAA
427	M N S L R A E D T A V Y Y C A K $\overline{\text{D}}$ R Y I T L P N ATGAACAGCCTGAGAGACAGCCGTTATTACTGTGCCAAAGACCGCTACATCACGTTGCCGAA
498	A L D Y W G Q G T L V T V L E G T G G S G T CGCGTTGGATTACTGGGGCCAGGGCACCCTGGTGACCGTGCTCGAGGGTACCGGAGGTTCCGGCGGAACCG
569	G S G T G T S E L D I Q M T Q S P V S L P V T P GGTCTGGGACTGGTACGAGGCTCGACATCCAGATGACCCAGTCTCCAGTCTCACTGCCCGTCACCCCT
640	G E P A S I S C R S S Q S L L H S N G Y N Y L D GGAGAGCCGGCCTCCATCTCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGA
711	W Y L Q K P G Q S P Q L L I Y L G S N R A S G TTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGG
782	V P D R F S G S G S G T D F T L K I S R V E A E TCCCTGACAGGTTCAGTGGCAGTGGATCAGGCAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAG
853	D V G V Y Y C Q Q Y K S N P P T F G Q G T K V E GATGTTGGGGTTATTACTGCCAGCAGTACAAGTCGAACCCGCCCACCTTCGGCCAGGGCACCAAAGTGGA
	NotI
024	I K R A A

	NCOI
72	M A E V Q L V E S G G CCATGGCCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGC
143	L V H P G G S L R L S C A G S G F T F S S Y A M TTGGTACATCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACCTTCAGTAGCTATGCTAT
214	H W V R Q A P G K G L E W V S A I G T G G G T GCACTGGGTTCGCCAGGCTCCAGGAAAAGGTCTGGAGTGGTATCAGCTATTGGTACCGGTGGTGGCACAT
285	Y Y A D S V Q G R F T I S R D N A K N S L Y L Q ACTATGCAGACTCCGTGCAGGGCCGATTCACCATCTCCAGAGACACTCCTTGTATCTTCAA
356	M N S L R A E D T A V Y Y C A R <u>Y D E P L T I Y</u> ATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCAAGATACGACGAGCCGCTGACGATTTA
427	W F D S W G Q G T L V T V S S G G G G S G G CTGGTTTGACTCCTGGGGCCAAGGTACCCTGGTCACCGTCTCGAGTGGTGGAGGCGGTTCAGGCGGAGGTG
498	G S G G G S E I E L T Q S P A T L S L S P G E GCTCTGGCGGTGGCGATCGGAAATTGAGCTCACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAA
569	R A T L S C R A S Q S V S S Y L A W Y Q Q K P G AGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGG
640	Q A P R L L I Y D A S N R A T G I P A R F S G CCAGGCTCCCAGGCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAG
711	S G S G T D F T L T I S S L E P E D F A V Y Y C GTGGGTCTGGGACAGACTTCACCCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGT
	Noti
782	Q Q R S N W P P A F G G G T K V E I K R A A CAGCAGCGTAGCAACTGGCCTCCGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACTGAGCACCCC

Figure 11

	NcoI
72	M A E V Q L V E CCATGGCCGAGGTGCAGCTGGAG
143	S G G G L V H P G G S L R L S C A G S G F T F S TCTGGGGGAGGCTTGGTACATCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACCTTCAG
214	S Y A M H W V R Q A P G K G L E W V S A I G T TAGCTATGCTATGCACTGGGTTCGCCAGGCTCCAGGAAAAGGTCTGGAGTGGGTATCAGCTATTGGTACTG
285	G G G T Y Y A D S V M G R F T I S R D N S K N T GTGGTGGCACATACTATGCAGACTCCGTGATGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG
3 56	L Y L Q M N S L R A E D T A V Y Y C A R <u>Y D N V</u> CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCAAGATACGACAATGT
427	M G L Y W F D Y W G Q G T L V T V S S G G G G G G G G G G G G G G G G G
498	S G G G G G G G G S E I E L T Q S P A T L S L CAGGCGGAGGTGGCTCTGGCGGATCGGAAATTGAGCTCACACAGTCTCCAGCCACCCTGTCTTTG
569	S P G E R A T L S C R A S Q S V S S Y L A W Y Q TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCA
640	Q K P G Q A P R L L I Y D A S N R A T G I P A ACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCA
711	R F S G S G S G T D F T L T I S S L E P E D F A GGTTCAGTGGCAGTGGGACAGACTTCACTCTCACCATCAGCAGCCTGAAGACTTTTGCA
782	V Y Y C Q Q R S N W P P A F G G G T K V E I K R GTTTATTACTGTCAGCAGCGTAGCAACTGGCCTCCGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACG
053	Noti À A

Figure 12



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Figure 13A

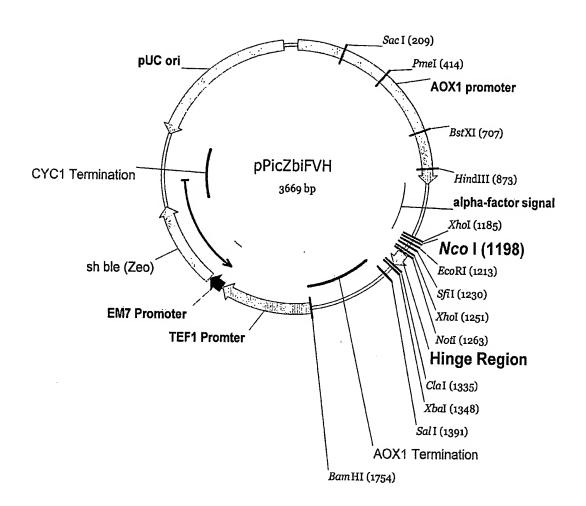
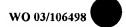
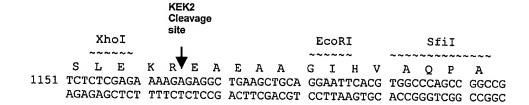


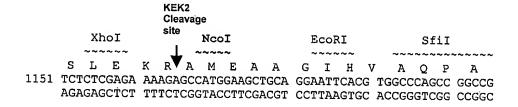
Figure 13B



5' Cloning site of pPicZαB

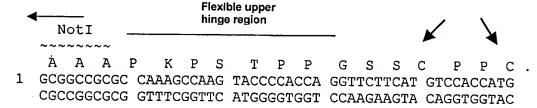


5' Cloning site of pPicZFVH



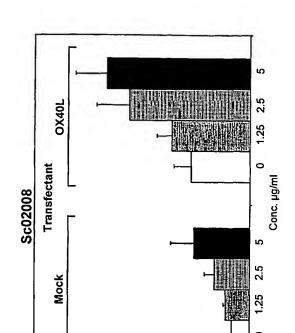
synthetic hinge fragment

Cysteine residues available for disulphide bonding



	Short linker						ClaI						XbaI			
	*4.**						~~~~~						~~~~~			
												G	_			
51	TCCAGGCTCT				GGCGGTGCGC			C	CAATCGATAG			CGGCTTTCTA		'CTA	GA	
	AGGTCCGAGA				CCGCCACGCG				GTTAG	CTA	TC	GCCGAAAGAT CT				

Figure 13C



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20000

30000

cpm 40000 10000

20000

80000

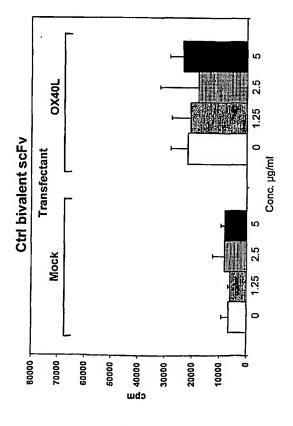


Figure 14A

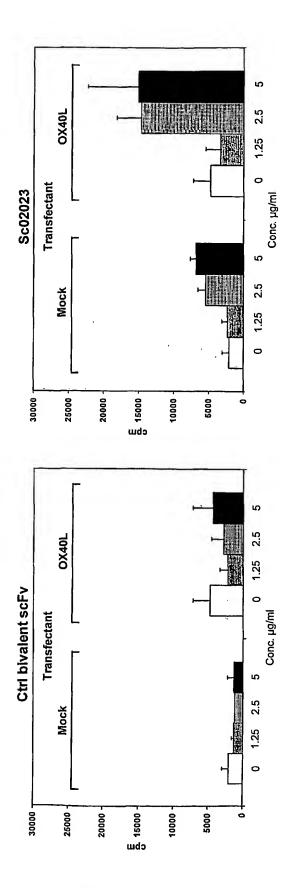


Figure 14B

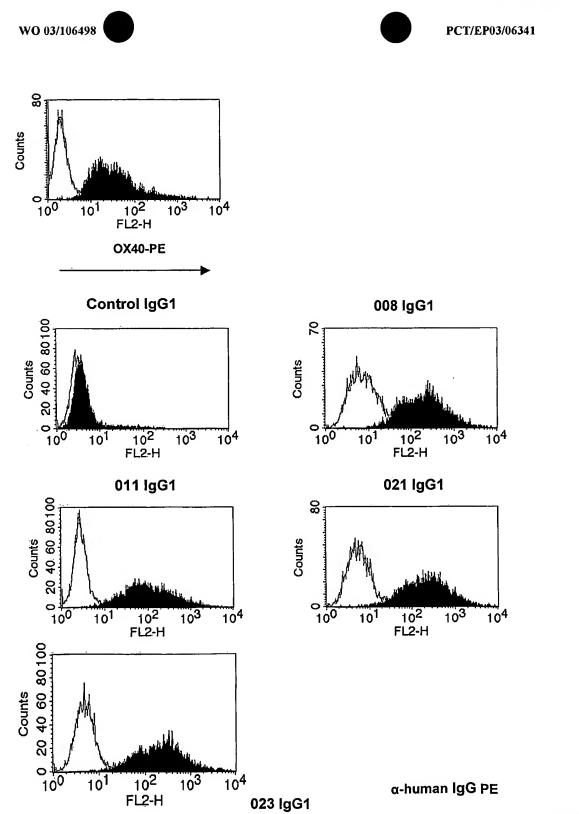


Figure 15